

FIGURE 1

05060605 070001

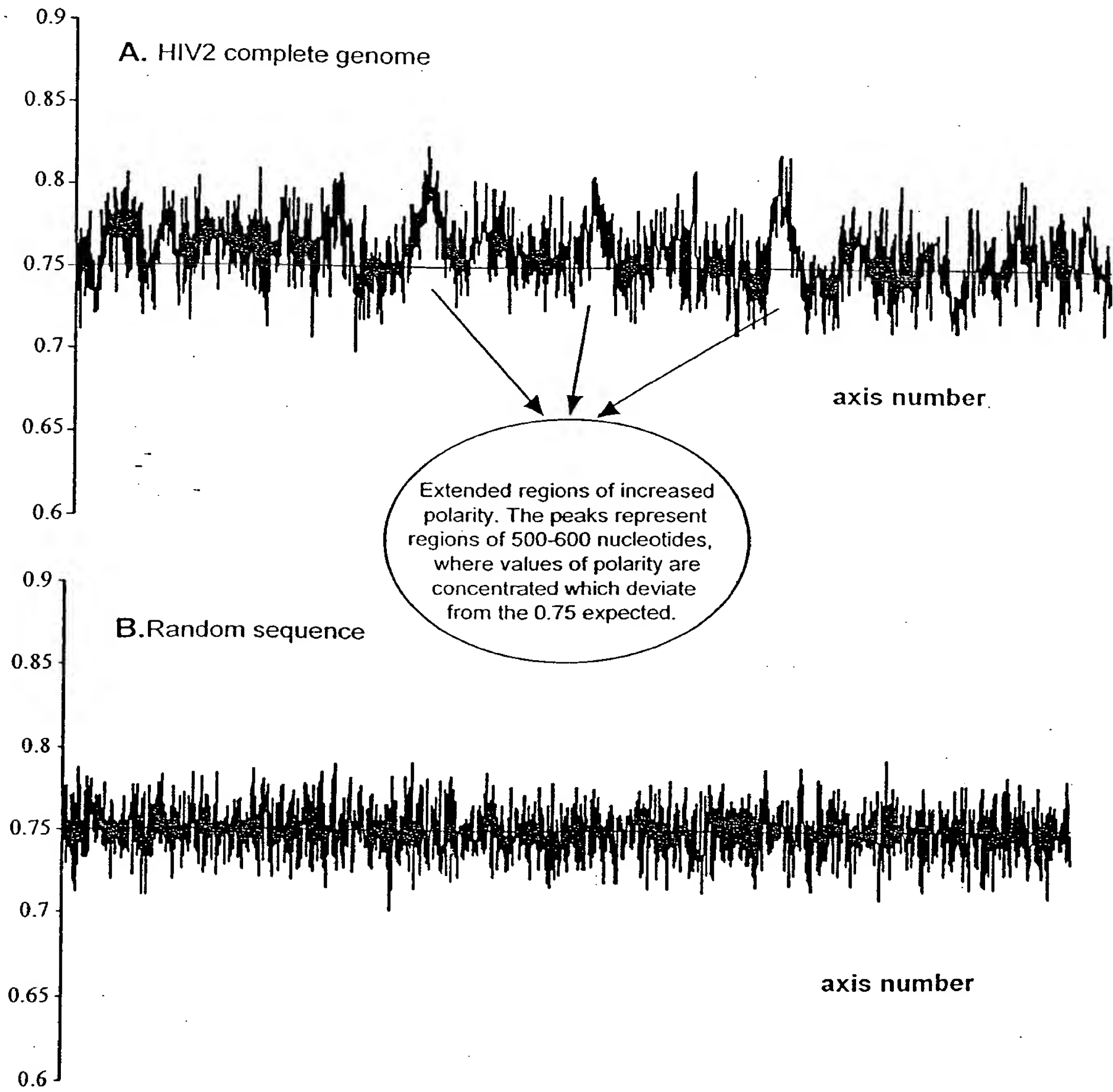
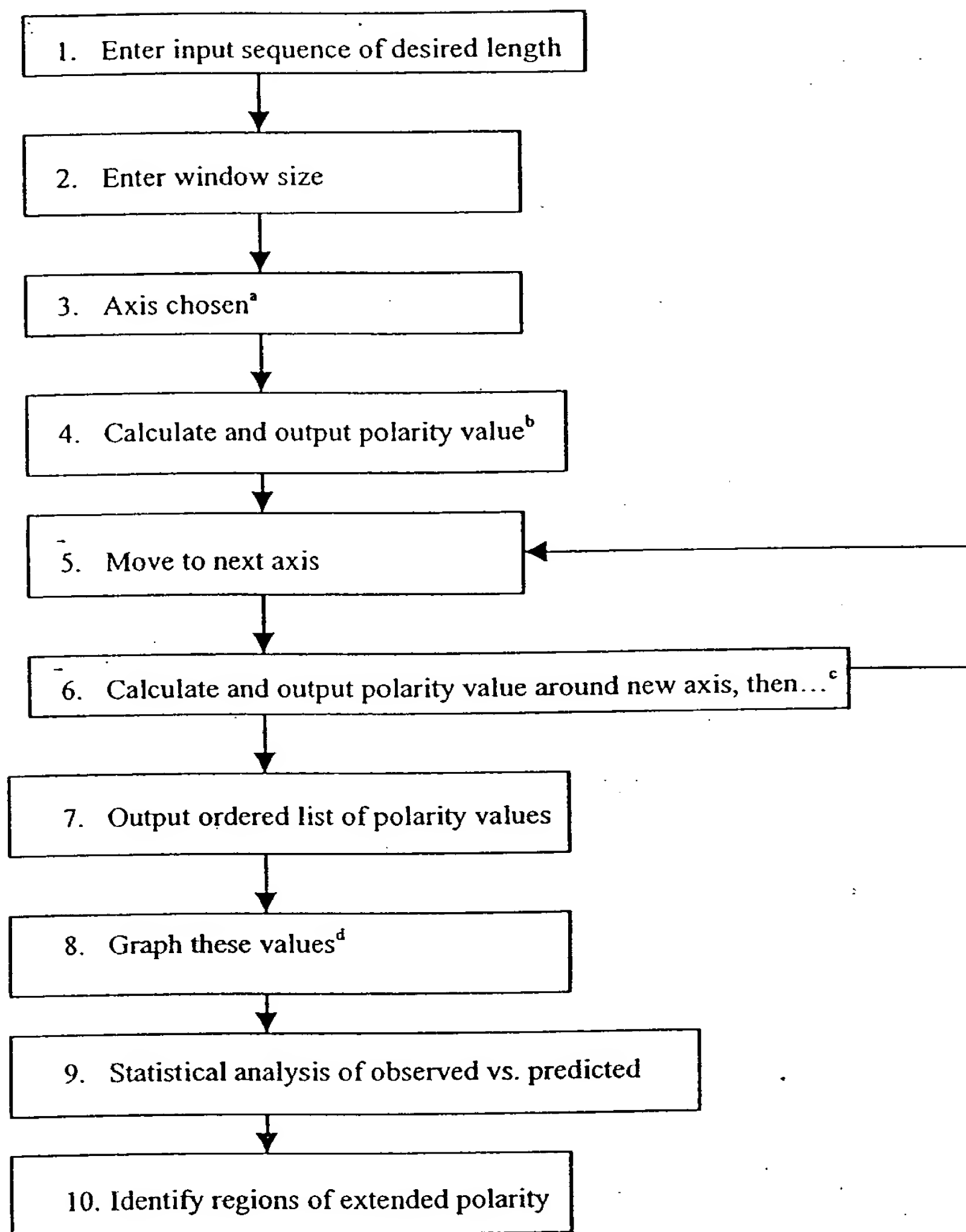


FIGURE 2



^a Starting at position = $(2 * \text{window of symmetry})$

^b $[1 - (S/W)]$

^c Up to and including axis position = $[2 * \text{length} - (2 * \text{window size})]$

^d Can use a moving average of values (with number of values averaged and increment of moving being variable) to smooth curve

FIGURE 3

The algorithm was implemented in PERL programming language.
 PERL variable-names and function-names are in boldface.

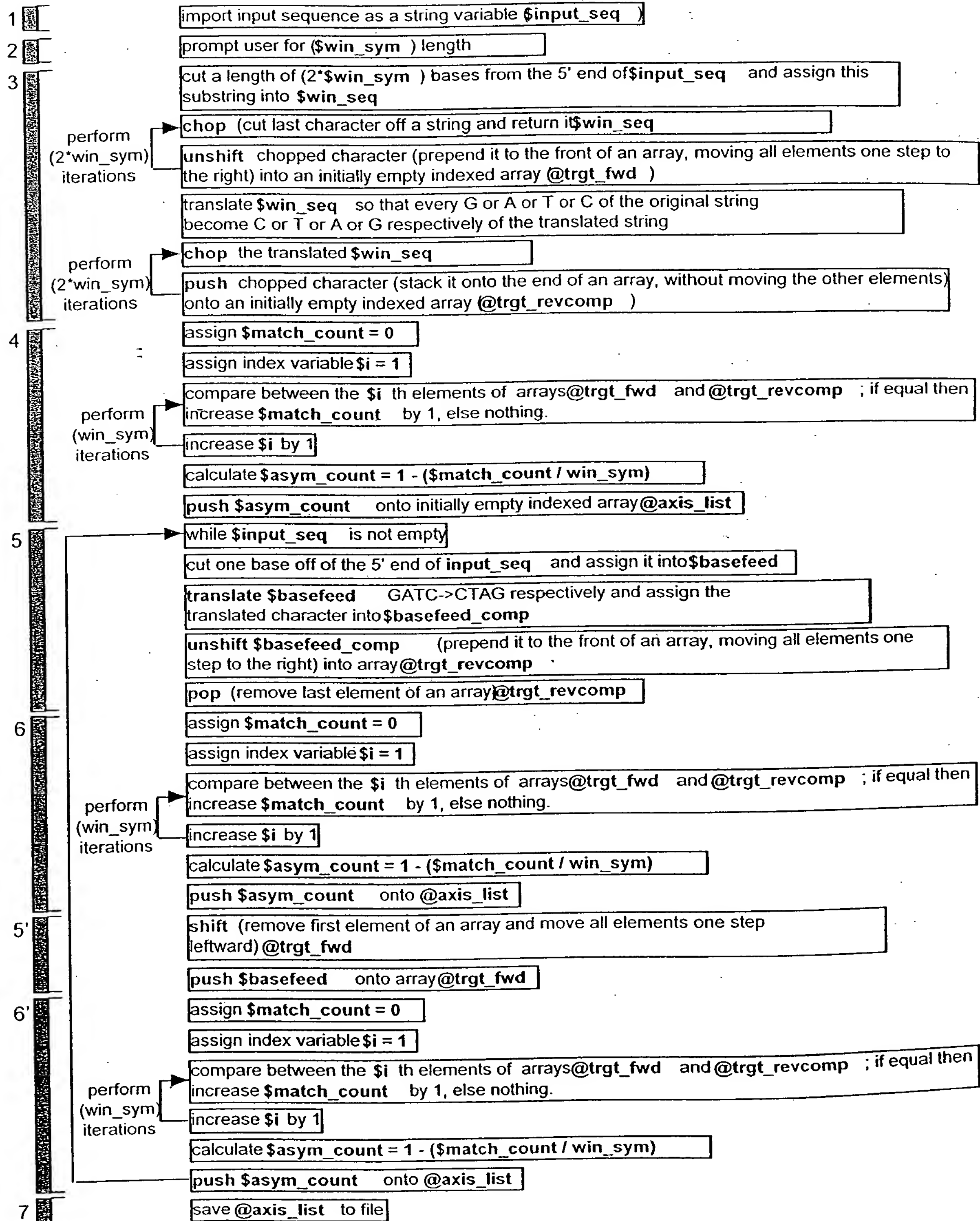


FIGURE 4

00000000000000000000000000000000



Figure 1 displays a series of 10 stacked line plots, each representing a different gene or control. The y-axis for all plots is the number of residual dead pairs, ranging from -20 to 40. The x-axis represents the chi-squared value, ranging from -100 to 400. The genes shown are FMR1, WRN, pou4f3, ATM, RB, NPC1, CFTR, HEXA, HD, and a random control (Rand 40k). Each plot shows a noisy signal with a dashed line indicating a trend. Circled points with arrows highlight specific peaks or features for each gene.

FIGURE 8

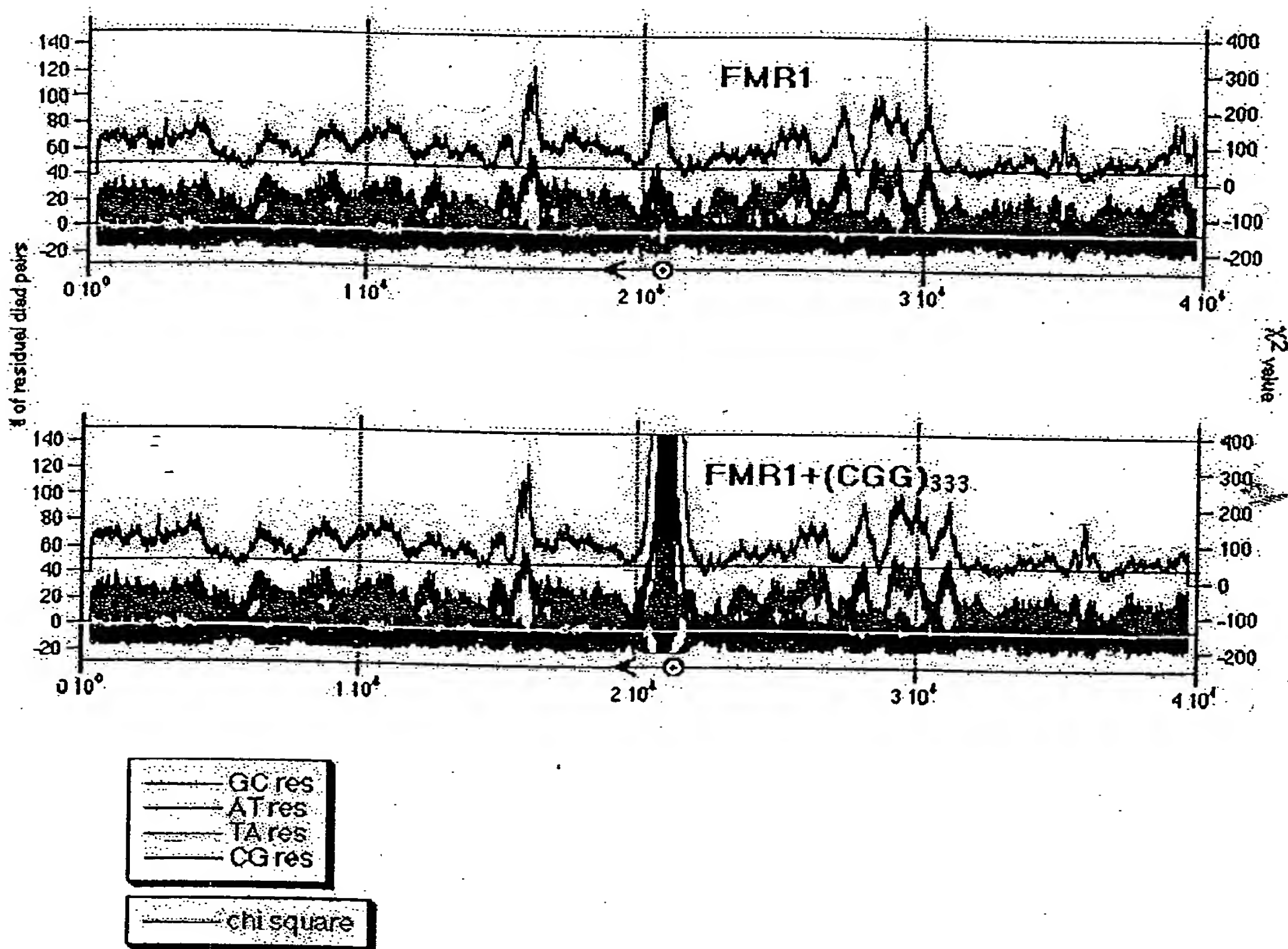


FIGURE 9

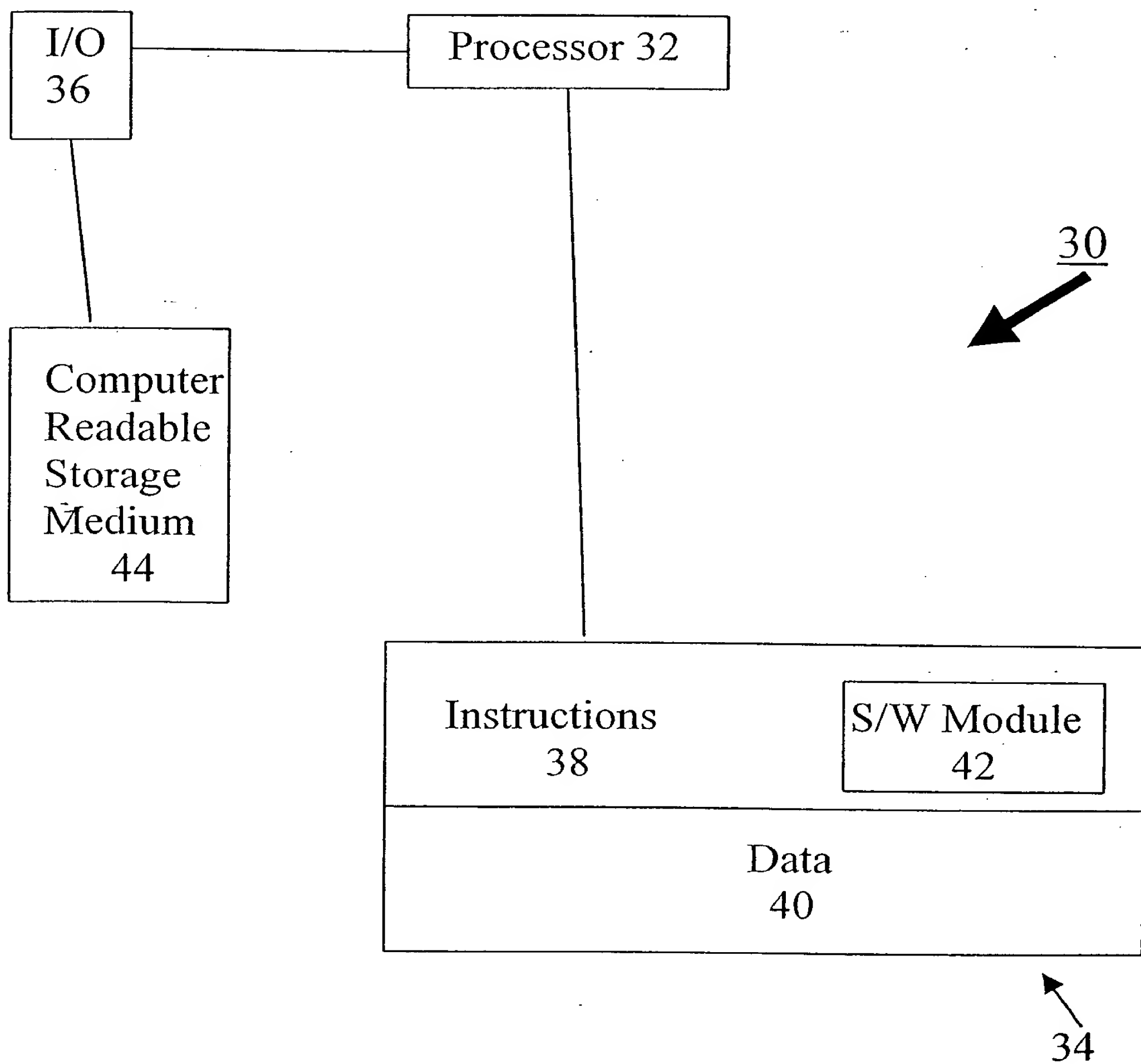


FIGURE 10